

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/155, 574D

Source: IFW/6

Date Processed by STIC: 6/2/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 06/02/2005

PATENT APPLICATION: US/09/155,514D

TIME: 09:04:16

Input Set : A:\1102-98.txt

Output Set: N:\CRF4\06022005\I155514D.raw

```

4 <110> APPLICANT: Kainoh, Mie
5   Tanaka, Toshiaki
7 <120> TITLE OF INVENTION: Chimeric Proteins, their Heterodimer
8   Complexes, and Platelet Substitutes
12 <130> FILE REFERENCE: 1102-98
14 <140> CURRENT APPLICATION NUMBER: 09/155,514D
15 <141> CURRENT FILING DATE: 1998-11-17
17 <150> PRIOR APPLICATION NUMBER: WO PCT/JP98/00370
18 <151> PRIOR FILING DATE: 1998-01-29
20 <150> PRIOR APPLICATION NUMBER: JP 9-15118
21 <151> PRIOR FILING DATE: 1997-01-29
23 <150> PRIOR APPLICATION NUMBER: JP-9-234544
24 <151> PRIOR FILING DATE: 1997-08-29
26 <160> NUMBER OF SEQ ID NOS: 34
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 4228
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: sequence encoding fusion protein
W--> 38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)...(2958)
W--> 41 <221> CDS
42 <222> LOCATION: (3316)...(3360)
W--> 44 <221> CDS
45 <222> LOCATION: (3480)...(3808)
W--> 47 <221> CDS
48 <222> LOCATION: (3904)...(4228)
W--> 50 <400> 1
51 atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg   48
52 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
53 1           5           10           15
55 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg   96
56 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
57           20           25           30
59 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg   144
60 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
61           35           40           45
63 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg   192
64 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
65           50           55           60
67 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc   240

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68 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
69 65 70 75 80
71 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga 288
72 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
73 85 90 95
75 tgc agg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg 336
76 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
77 100 105 110
79 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga 384
80 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
81 115 120 125
83 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat 432
84 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
85 130 135 140
87 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata 480
88 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
89 145 150 155 160
91 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct 528
92 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
93 165 170 175
95 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat 576
96 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
97 180 185 190
99 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata 624
100 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
101 195 200 205
103 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca 672
104 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
105 210 215 220
107 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa 720
108 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
109 225 230 235 240
111 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat 768
112 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
113 245 250 255
115 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc 816
116 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
117 260 265 270
119 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat 864
120 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
121 275 280 285
123 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa 912
124 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
125 290 295 300
127 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgt gct gtg gac 960
128 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
129 305 310 315 320
131 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag 1008
132 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln

```

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133		325		330		335		
135	agc acc atc	aga gag gaa gga	aga gtg ttt	gtg tac atc	aac tct ggc	1056		
136	Ser Thr Ile	Arg Glu Glu Gly	Arg Val Phe	Val Tyr Ile	Asn Ser Gly			
137		340		345	350			
139	tcg gga gca	gta atg aat gca	atg gaa aca	aac ctc gtt	gga agt gac	1104		
140	Ser Gly Ala	Val Met Asn Ala	Met Glu Thr	Asn Leu Val	Gly Ser Asp			
141		355		360	365			
143	aaa tat gct	gca aga ttt ggg	gaa tct ata	gtt aat ctt	ggc gac att	1152		
144	Lys Tyr Ala	Ala Arg Phe Gly	Glu Ser Ile	Val Asn Leu	Gly Asp Ile			
145		370		375	380			
147	gac aat gat	ggc ttt gaa	gat gtt gct	atc gga gct	cca caa gaa	gat	1200	
148	Asp Asn Asp	Gly Phe Glu	Asp Val Ala	Ile Gly Ala	Pro Gln Glu	Asp		
149	385		390		395	400		
151	gac ttg caa	ggt gct att	tat att tac	aat ggc cgt	gca gat ggg	atc	1248	
152	Asp Leu Gln	Gly Ala Ile	Tyr Ile Tyr	Asn Gly Arg	Ala Asp Gly	Ile		
153		405		410	415			
155	tcg tca acc	ttc tca cag	aga att gaa	gga ctt cag	atc agc aaa	tcg	1296	
156	Ser Ser Thr	Phe Ser Gln	Arg Ile Glu	Gly Leu Gln	Ile Ser Lys	Ser		
157		420		425	430			
159	tta agt atg	ttt gga cag	tct ata tca	gga caa att	gat gca gat	aat	1344	
160	Leu Ser Met	Phe Gly Gln	Ser Ile Ser	Gly Gln Ile	Asp Ala Asp	Asn		
161		435		440	445			
163	aat ggc tat	gta gat gta	gca gtt ggt	gct ttt cgg	tct gat tct	gct	1392	
164	Asn Gly Tyr	Val Asp Val	Ala Val Gly	Ala Phe Arg	Ser Asp Ser	Ala		
165		450		455	460			
167	gtc ttg cta	agg aca aga	cct gta gta	att gtt gac	gct tct tta	agc	1440	
168	Val Leu Leu	Arg Thr Arg	Pro Val Val	Ile Val Asp	Ala Ser Leu	Ser		
169	465		470		475	480		
171	cac cct gag	tca gta aat	aga acg aaa	ttt gac tgt	gtt gaa aat	gga	1488	
172	His Pro Glu	Ser Val Asn	Arg Thr Lys	Phe Asp Cys	Val Glu Asn	Gly		
173		485		490	495			
175	tgg cct tct	gtg tgc ata	gat cta aca	ctt tgt ttc	tca tat aag	ggc	1536	
176	Trp Pro Ser	Val Cys Ile	Asp Leu Thr	Leu Cys Phe	Ser Tyr Lys	Gly		
177		500		505	510			
179	aag gaa gtt	cca ggt tac	att gtt ttg	ttt tat aac	atg agt ttg	gat	1584	
180	Lys Glu Val	Pro Gly Tyr	Ile Val Leu	Phe Tyr Asn	Met Ser Leu	Asp		
181		515		520	525			
183	gtg aac aga	aag gca gag	tct cca cca	aga ttc tat	ttc tct tct	aat	1632	
184	Val Asn Arg	Lys Ala Glu	Ser Pro Pro	Arg Phe Tyr	Phe Ser Ser	Asn		
185		530		535	540			
187	gga act tct	gac gtg att	aca gga agc	ata cag gtg	tcc agc aga	gaa	1680	
188	Gly Thr Ser	Asp Val Ile	Thr Gly Ser	Ile Gln Val	Ser Ser Arg	Glu		
189	545		550		555	560		
191	gct aac tgt	aga aca cat	caa gca ttt	atg cgg aaa	gat gtg cgg	gac	1728	
192	Ala Asn Cys	Arg Thr His	Gln Ala Phe	Met Arg Lys	Asp Val Arg	Asp		
193		565		570	575			
195	atc ctc acc	cca att cag	att gaa gct	gct tac cac	ctt ggt cct	cat	1776	
196	Ile Leu Thr	Pro Ile Gln	Ile Glu Ala	Ala Tyr His	Leu Gly Pro	His		
197		580		585	590			

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199	gtc	atc	agt	aaa	cga	agt	aca	gag	gaa	ttc	cca	cca	ctt	cag	cca	att	1824
200	Val	Ile	Ser	Lys	Arg	Ser	Thr	Glu	Glu	Phe	Pro	Pro	Leu	Gln	Pro	Ile	
201			595					600					605				
203	ctt	cag	cag	aag	aaa	gaa	aaa	gac	ata	atg	aaa	aaa	aca	ata	aac	ttt	1872
204	Leu	Gln	Gln	Lys	Lys	Glu	Lys	Asp	Ile	Met	Lys	Lys	Thr	Ile	Asn	Phe	
205		610					615					620					
207	gca	agg	ttt	tgt	gcc	cat	gaa	aat	tgt	tct	gct	gat	tta	cag	gtt	tct	1920
208	Ala	Arg	Phe	Cys	Ala	His	Glu	Asn	Cys	Ser	Ala	Asp	Leu	Gln	Val	Ser	
209	625					630					635					640	
211	gca	aag	att	ggg	ttt	ttg	aag	ccc	cat	gaa	aat	aaa	aca	tat	ctt	gct	1968
212	Ala	Lys	Ile	Gly	Phe	Leu	Lys	Pro	His	Glu	Asn	Lys	Thr	Tyr	Leu	Ala	
213					645						650					655	
215	gtt	ggg	agt	atg	aag	aca	ttg	atg	ttg	aat	gtg	tcc	ttg	ttt	aat	gct	2016
216	Val	Gly	Ser	Met	Lys	Thr	Leu	Met	Leu	Asn	Val	Ser	Leu	Phe	Asn	Ala	
217				660					665					670			
219	gga	gat	gat	gca	tat	gaa	acg	act	cta	cat	gtc	aaa	cta	ccc	gtg	ggc	2064
220	Gly	Asp	Asp	Ala	Tyr	Glu	Thr	Thr	Leu	His	Val	Lys	Leu	Pro	Val	Gly	
221			675					680					685				
223	ctt	tat	ttc	att	aag	att	tta	gag	ctg	gaa	gag	aag	caa	ata	aac	tgt	2112
224	Leu	Tyr	Phe	Ile	Lys	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Gln	Ile	Asn	Cys	
225		690					695					700					
227	gaa	gtc	aca	gat	aac	tct	ggc	gtg	gta	caa	ctt	gac	tgc	agt	att	ggc	2160
228	Glu	Val	Thr	Asp	Asn	Ser	Gly	Val	Val	Gln	Leu	Asp	Cys	Ser	Ile	Gly	
229	705					710					715					720	
231	tat	ata	tat	gta	gat	cat	ctc	tca	agg	ata	gat	att	agc	ttt	ctc	ctg	2208
232	Tyr	Ile	Tyr	Val	Asp	His	Leu	Ser	Arg	Ile	Asp	Ile	Ser	Phe	Leu	Leu	
233					725					730					735		
235	gat	gtg	agc	tca	ctc	agc	aga	gcg	gaa	gag	gac	ctc	agt	atc	aca	gtg	2256
236	Asp	Val	Ser	Ser	Leu	Ser	Arg	Ala	Glu	Glu	Asp	Leu	Ser	Ile	Thr	Val	
237				740					745					750			
239	cat	gct	acc	tgt	gaa	aat	gaa	gag	gaa	atg	gac	aat	cta	aag	cac	agc	2304
240	His	Ala	Thr	Cys	Glu	Asn	Glu	Glu	Glu	Met	Asp	Asn	Leu	Lys	His	Ser	
241			755					760					765				
243	aga	gtg	act	gta	gca	ata	cct	tta	aaa	tat	gag	gtt	aag	ctg	act	gtt	2352
244	Arg	Val	Thr	Val	Ala	Ile	Pro	Leu	Lys	Tyr	Glu	Val	Lys	Leu	Thr	Val	
245		770					775						780				
247	cat	ggg	ttt	gta	aac	cca	act	tca	ttt	gtg	tat	gga	tca	aat	gat	gaa	2400
248	His	Gly	Phe	Val	Asn	Pro	Thr	Ser	Phe	Val	Tyr	Gly	Ser	Asn	Asp	Glu	
249	785					790					795					800	
251	aat	gag	cct	gaa	acg	tgc	atg	gtg	gag	aaa	atg	aac	tta	act	ttc	cat	2448
252	Asn	Glu	Pro	Glu	Thr	Cys	Met	Val	Glu	Lys	Met	Asn	Leu	Thr	Phe	His	
253					805						810					815	
255	gtt	atc	aac	act	ggc	aat	agt	atg	gct	ccc	aat	gtt	agt	gtg	gaa	ata	2496
256	Val	Ile	Asn	Thr	Gly	Asn	Ser	Met	Ala	Pro	Asn	Val	Ser	Val	Glu	Ile	
257				820						825						830	
259	atg	gta	cca	aat	tct	ttt	agc	ccc	caa	act	gat	aag	ctg	ttc	aac	att	2544
260	Met	Val	Pro	Asn	Ser	Phe	Ser	Pro	Gln	Thr	Asp	Lys	Leu	Phe	Asn	Ile	
261			835					840						845			
263	ttg	gat	gtc	cag	act	act	act	gga	gaa	tgc	cac	ttt	gaa	aat	tat	caa	2592

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```

264 Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
265      850      855      860
267 aga gtg tgt gca tta gag cag caa aag agt gca atg cag acc ttg aaa 2640
268 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
269 865      870      875      880
271 ggc ata gtc cgg ttc ttg tcc aag act gat aag agg cta ttg tac tgc 2688
272 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
273      885      890      895
275 ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa 2736
276 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
277      900      905      910
279 atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg 2784
280 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
281      915      920      925
283 cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata 2832
284 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
285      930      935      940
287 aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac 2880
288 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
289 945      950      955      960
291 aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa 2928
292 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
293      965      970      975
295 aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaag caggctcagc 2978
296 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu
297      980      985
299 gctcctgcct ggacgcatcc cggtatgca gccccagtc agggcagcaa ggcaggcccc 3038
300 gtctgcctct tcacccggag cctctgccc cccactcat gctcaggag agggctcttct 3098
301 ggctttttcc caggctctgg gcaggcacag gctagggtgcc cctaaccag gccctgcaca 3158
302 caaaggggca ggtgctgggc tcagacctgc caagagccat atccgggag accctgcccc 3218
303 tgacctaaagc ccaccccaaa ggccaaactc tccactccct cagctcggac accttctctc 3278
304 ctcccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac 3333
305      Glu Pro Lys Ser Cys Asp
306      990
308 aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc 3380
309 Lys Thr His Thr Cys Pro Pro Cys Pro
310      995      1000
312 gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcattccagg gacaggcccc 3440
313 agccgggtgc tgacacgtcc acctccatct ctctctcag cac ctg aac tcc tgg 3494
314      His Leu Asn Ser Trp
315      1005
317 ggg gac cgt cag tct tcc tct tcc ccc caa aac cca agg aca ccc tca 3542
318 Gly Asp Arg Gln Ser Ser Ser Ser Pro Gln Asn Pro Arg Thr Pro Ser
319      1010      1015      1020
321 tga tct ccc gga ccc ctg agg tca cat gcg tgg tgg tgg acg tga gcc 3590
322 * Ser Pro Gly Pro Leu Arg Ser His Ala Trp Trp Trp Thr * Ala
323      1025      1030      1035
325 acg aag acc ctg agg tca agt tca act ggt acg tgg acg gcg tgg agg 3638
326 Thr Lys Thr Leu Arg Ser Ser Ser Thr Gly Thr Trp Thr Ala Trp Arg

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L:38 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:50 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:387 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:855 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:858 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
L:861 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
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L:867 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19